

Figure 1

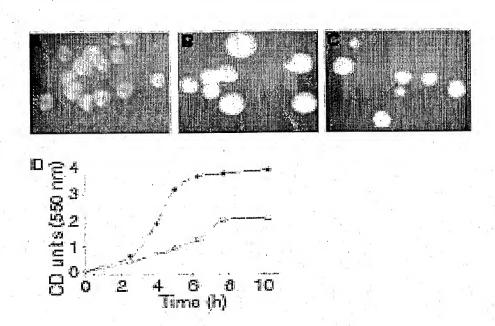


Figure 2

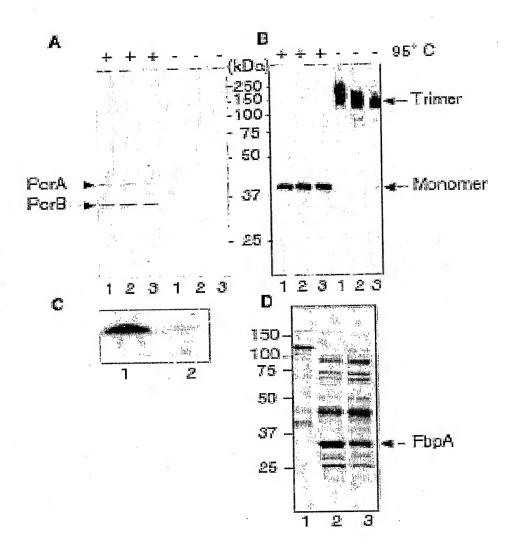


Figure 3

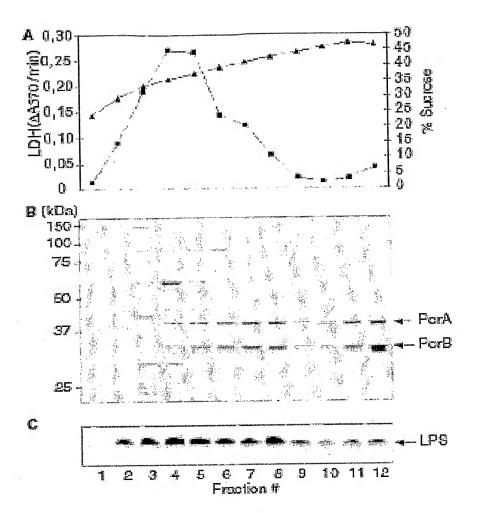


Figure 4

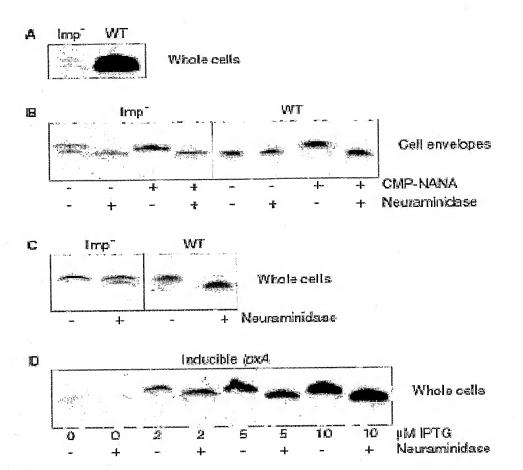


Figure 5

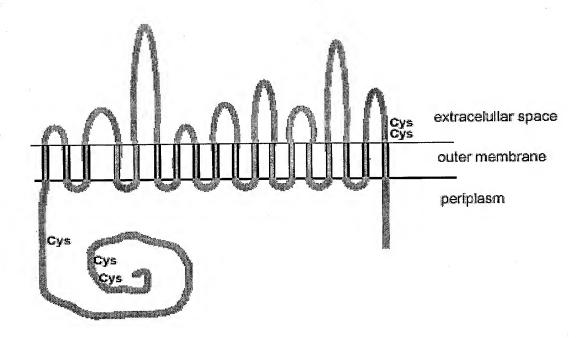


Figure 6

Imp/OstA - SEQ ID No 1
Predicted extracellular loops are indicated in bold

LARLFSLKPLVLALGLCFGTHCAAADAVAAEETDNPTAGESVRSVSEPIQPTSLSLGSTC
LFCSNESGSPERTEAAVQGSGEASIPEDYTRIVADRMEGQSQVQVRAEGNVVVERNRTTL 120
NTDWADYDQSGDTVTAGDRFALQQDGTLIRGETLTYNLEQQTGEAHNVRMEIEQGGRRLQ 180
SVSRTAEMLGEGHYKLTETQFNTCSAGDAGWYVKAASVEADREKGIGVAKHAAFVFGGVP 240
IFYTPWADFPLDGNRKSGLLVPSLSAGSDGVSLSVPYYFNLAPNLDATFAPSVIGERGAV 300
FDGQVRYLRPDYAGQSDLTWLPHDKKSGRNNRYQAKWQHRHDISDTLQAGVDFNQVSDSG 360
YYRDFYGNKEIAGNVNLNRRVWLDYGGRAAGGSLNAGLSVLKYQTLANQSGYKDKPYALM 420
PRLSVEWRKNTGRAQIGVSAQFTRFSHDSRQDGSRLVVYPDIKWDFSNSWGYVRPKLGLH 480
ATYYSLNRFGSQEARRVSRTLPIVNIDSGATFERNTRMFGGEVLQTLEPRLFYNYIPAKS 540
QNDLPNFDSSESSFGYGQLFRENLYYGNDRINTANSLSAAVQSRILDGATGEERFRAGIG 600
QKFYFKDDAVMLDGSVGKKPRNRSDWVAFASGSIGSRFILDSSIHYNQNDKRAENYAVGA 660
SYRPAQGKVLNARYKYGRNEKIYLKSDGSYFYDKLSQLDLSAQWPLTRNLSAVVRYNYGF 720
EAKKPIEVLAGAEYKSSCGCWGAGVYAQRYVTGENTYKNAVFFSLQLKDLSSVGRNPADR 780

loop 1: 252-271 loop 2: 295-332 loop 3: 357-416 loop 4: 444-455 loop 5: 482-501 loop 6: 537-576 loop 7: 606-624 loop 8: 648-697 loop 9: 721-740

Figure 7

Imp-FAM18 NMB0280 NMA2207	LARLFSLKPLVLALGFCFGTHCAAADAVAAEETDNPTAGGSVRSVSEPIQPTSLSLGSTC LARLFSLKPLVLALGLCFGTHCAAADAVAAEETDNPTAGESVRSVSEPIQPTSLSLGSTC MARLFSLKPLVLALGFCFGTHCAAADAVAAEETDNPTAGGSVRSVSEPIQPTSLSLGSTC :************************************	60 60
Imp-FAM18 NMB0280 NMA2207	LFCSNESGSPERTEAAVRGSGEASIPEDYTRIVADKVEGQSQVQVRAEGNVVVERNRTTL LFCSNESGSPERTEAAVQGSGEASIPEDYTRIVADRMEGQSQVQVRAEGNVVVERNRTTL LFCSNESGSPERTEAAVQGSGEASIPEDYTRIVADRMEGQSQVQVRAEGNVVVERNRTTL ***********************************	120 120
Imp-FAM18 NMB0280 NMA2207	NTDWADYDQSGDTVTAGDRFALQQDGTLIRGETLTYNLEQQTGEAHNVRMETEHGGRRLQ NTDWADYDQSGDTVTAGDRFALQQDGTLIRGETLTYNLEQQTGEAHNVRMEIEQGGRRLQ NADWADYDQSGDTVTAGDRFALQQDGTLIRGETLTYNLEQQTGEAHNVRMETEHGGRRLQ *:***********************************	180 180 180
Imp-FAM18 NMB0280 NMA2207	SVSRTAEMLGEGHYKLTETQFNTCSAGDAGWYVKAASVEADREKGIGVAKHAAFVFGGVP SVSRTAEMLGEGHYKLTETQFNTCSAGDAGWYVKAASVEADREKGIGVAKHAAFVFGGVP SVSRTAEMLGEGHYKLTETQFNTCSAGDAGWYVKAASVEADREKGIGVAKHAAFVFGGVP ***********************************	240 240 240
Imp-FAM18 NMB0280 NMA2207	IFYTPWADFPLDGNRKSGLLVPSLSAGSDGVSLSVPYYFNLAPNLDATFAPSVIGERGAV IFYTPWADFPLDGNRKSGLLVPSLSAGSDGVSLSVPYYFNLAPNLDATFAPSVIGERGAV IFYTPWADFPLDGNRKSGLLVPSLSAGSDGVSLSVPYYFNLAPNLDATFAPGVIGERGAV ************************************	300 300 300
Imp-FAM18 NMB0280 NMA2207	FDGQVRYLRPDYAGQSDLTWLPHDKKSGRNNRYQAKWQHRHDISDTLQAGVDFNQVSDSG FDGQVRYLRPDYAGQSDLTWLPHDKKSGRNNRYQAKWQHRHDISDTLQAGVDFNQVSDSG FDGQVRYLRPDYAGQSDLTWLPHDKKSGRNNRYQAKWQHRHDISDTLQAGVDFNQVSDSG ***********************************	360 360 360
Imp-FAM18 NMB0280 NMA2207	YYRDFYGNKEIAGNVNLNRRVWLDYGGRAAGGSLNAGLSVLKYQTLANQSGYKDKPYALM YYRDFYGNKEIAGNVNLNRRVWLDYGGRAAGGSLNAGLSVLKYQTLANQSGYKDKPYALM YYRDFYGNKEIAGNVNLNRRVWLDYGGRAAGGSLNAGLSVLKYQTLANQSGYKDKPYALM ************************************	420 420 420
Imp-FAM18 NMB0280 NMA2207	PRLSADWRKNTGRAQIGVSAQFTRFSHDSRQDGSRLVVYPDIKWDFSNSWGYVRPKLGLH PRLSVEWRKNTGRAQIGVSAQFTRFSHDSRQDGSRLVVYPDIKWDFSNSWGYVRPKLGLH PRLSADWRKNTGRAQIGVSAQFTRFSHDSRQDGSRLVVYPDIKWDFSNSWGYVRPKLGLH ****.:********************************	480
Imp-FAM18 NMB0280 NMA2207	ATYYSLNRFGSQEARRVSRTLPIVNIDSGATFERNTRMFGGGVLQTLEPRLFYNYIPAKS ATYYSLNRFGSQEARRVSRTLPIVNIDSGATFERNTRMFGGEVLQTLEPRLFYNYIPAKS ATYYSLNRFGSQEARRVSRTLPIVNIDSGMTFERNTRMFGGGVLQTLEPRLFYNYIPAKS ************************************	540 540 540
Imp-FAM18 NMB0280 NMA2207	QNDLPNFDSSESSFGYGQLFRENLYYGNDRINTANSLSAAVQSRILDGATGEERFRAGIG QNDLPNFDSSESSFGYGQLFRENLYYGNDRINTANSLSAAVQSRILDGATGEERFRAGIG QNDLPNFDSSESSFGYGQLFRENLYYGNDRINTANSLSAAVQSRILDGATGEERFRAGIG ***********************************	600 600 600
Imp-FAM18 NMB0280 NMA2207	QKFYFKDDAVMLDGSVGKKPRNRSDWVAFASGSIGSRFILDSSIHYNQNDKRAENYAVGA QKFYFKDDAVMLDGSVGKKPRNRSDWVAFASGSIGSRFILDSSIHYNQNDKRAENYAVGA QKFYFKNDAVMLDGSVGKKPRSRSDWVAFASSGIGSRFILDSSIHYNQNDKRAENYAVGA *****:*******************************	660
Imp-FAM18 NMB0280 NMA2207	SYRPAQGKVLNARYKYGRNEKIYLKSDGSYFYDKLSQLDLSAQWPLTRNLSAVVRYNYGF SYRPAQGKVLNARYKYGRNEKIYLKSDGSYFYDKLSQLDLSAQWPLTRNLSAVVRYNYGF SYRPAQGKVLNARYKYGRNEKIYLKSDGSYFYDKLSQLDLSAQWPLTRNLSAVVRYNYGF	720
Imp-FAM18 NMB0280 NMA2207	EAKKPIEMLAGAEYKSSCGCWGAGVYAQRYVTGENTYKNAVFFSLQLKDLSSVGRNPADR EAKKPIEVLAGAEYKSSCGCWGAGVYAQRYVTGENTYKNAVFFSLQLKDLSSVGRNPADR EAKKPIEVLAGAEYKSSCGCWGAGVYAQRYVTGENTYKNAVFFSLQLKDLSSVGRNPADR ******:******************************	780
Imp-FAM18 NMB0280 NMA2207	MDVAVPGYIPAHSLSAGRNKRP 802 MDVAVPGYITAHSLSAGRNKRP 802 MDVAVPGYIPAHSLSAGRNKRP 802 ************************************	

Figure 8

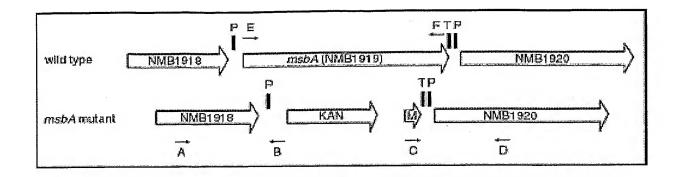


Figure 9

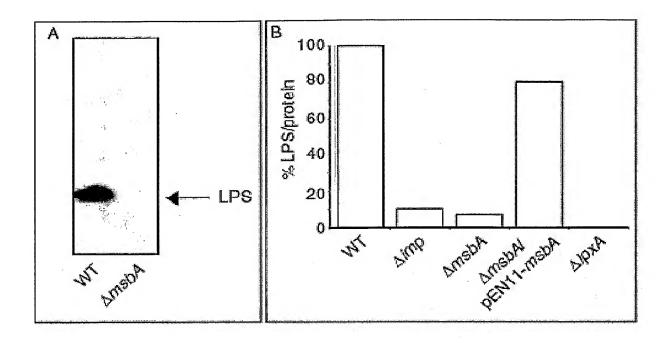


Figure 10

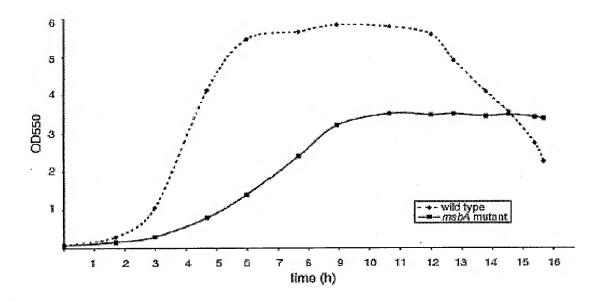


Figure 11

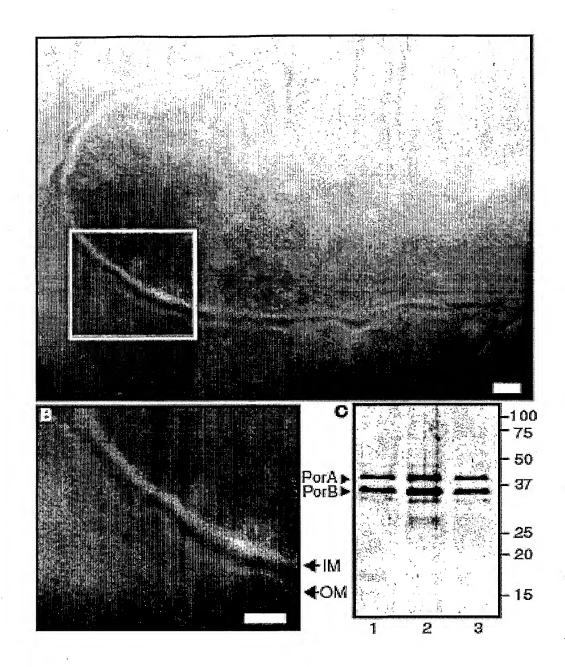


Figure 12

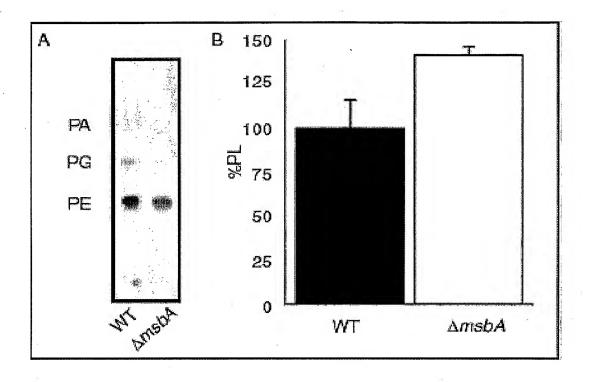


Figure 13

Α

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В

 ${\tt MLAWRPGRPDGCQAAGGRRYNPGHDCIKASVSLNSAARNAPAGSQPVKAELWKRVYSRVGSYWKGLVLAVLLMAGAAATQ}$

PTLAVIMKPLLDDGFSGAKPHYVWFLPLAVVGLILLRGICNFFSDYLLAWVANNVLRGIRGEMFERLLG LPDADFKRGDT

 ${\tt GRLLNRFTIDAGNVTGYATDVITVLVRETLVVIALIGVLLYMSWALTLIILVMLPVSVGIARAFTRRLR} \\ {\tt RINRETVNMNA}$

 $\verb|ELTRVVSEGIDGQRVIKLFDGYDAERRRFDFVNSRLRRFAMRSATADAALTPLTQVCISVAVGAVIAVA LSQANSGALTV|$

 ${\tt GSFASFMAALAQIFDPIKRLTNLAGKMQKMLVAAESVFTLVDQTPEADAGTRALPEPVRGKVEFRAVSHR FPDADRDTVS}$

AVSFLVEPGQTVALVGRSGSGKTTLVNMLPRFVLPDGGDILFDDVPIQDLTLRSLRSHLSLVSQDVVLFDDTIAANVGYG

 ${\tt AGGTVDDARVRDALAAANLLEFVDGLPLGIHTPVGQNAARLSGGQRQRLAIARALIKNAPVLILDEATS}$ ${\tt ALDNESERQVQ}$

ASLERLMRGRTTLVIAHRLSTVQNADRIIVLDAGKIVEHGPHSELLAANGLYASLYNMQFRED

Figure 14

atgatagaaaaactgactttcggactgtttaaaaaaagaagacgcgcgcagctttatgcgc ctgatggcgtacgtccgccctacaaaatccgcatcgttgccgccctgattgccattttc qqcqttqccqccaccgaaagctaccttgccqccttcatcqcccccctgattaaccacggc ttttccqcacctgccgcccccqaqctqtctgccgccgccggcatcatttccaccctg caaaactggcgcgaacagtttacctatatggtttgggggacggaaaacaaaatctggacc qtcccqctcttcctcatcatcctcgtcgtcatccgtggcatctgccgctttaccagcacc tatctqatgacttgggtctccgtgatgaccatcagcaaaatccgcaaagatatgtttgcc aaaatgctgaccctttcctcccgctaccatcaggaaacgccgtccggcaccgtactgatg aatatgctcaacctgaccgaacagtcggtcagcaacgccagcgacatcttcaccgtcctc acgcgcgacacgatgatcgttaccggcctgaccatcgtcctgctttacctcaactggcag ctcagcctcatcgtcgtcctgatgttccccctgctctccctgctctcgcgctactaccgc gaccgtctgaaacacgtcatttccgactcgcaaaaaagcataggcacgatgaacaacgtg attqccgaaacccatcagggacaccgcgtcgtcaagctgttcaacgggcaggcgcaggcg qcaaaccqqttcgacqcgqtcaaccqcaccatcqtccgcctcagcaaaaaaatcacgcag gcaacggcggcacattccccgttcagcgaactgatcgcctcgatcgccctcgccgtcgtc atcttcatcgccctgtggcaaagccaaaacggctacaccaccatcggcgaatttatggca ttcatcgtcgcgatgctgcaaatgtacgccccatcaaaagccttgccaacatcagcatc cctatgcagacgatgttcctcgccgccgacggtgtatgtgcatttctcgacaccccgccc gaacaggacaagggcacgctcgcaccgcagcgtgtcgaagggcgcatcagcttccgcaac gtcgatgtcgaataccgttcagacggcatcaaagccctcgacaacttcaacctcgacatc agacaaggcgaacgcgtcgccctggtcggacgttccggcagcggcaaatccaccgtcgtc aacctgctgccccgctttgtcgaaccgtctgccggcaacatctgcatagacggtatcgac atcgccgacatcaaactcgactgcctgcgcgcccaattcgccctcgtctcccaagacgta ttcctqtttqacqacaccctgtttgaaaacgtccgatacagccgtcccgacgcgggcgaa qccqaaqtcctgttcqccctccaaaccgccaacctgcaaagcctgattgacagctccccg ctcggactgcaccagcccatcggatcgaacggcagcaacttatccggcggacagcggcaa cgcgtcgccattgcccgcgccattttgaaagacgcgccgatattattattggacgaagcc accagegeattagacaacgaatcegaacgcetegteeaacaggegetegaacgcetgatg qaaaaccqcaccqqcatcatcqtcqcccaccqcctqaccaccatcqaaggggccgaccgc atcatcqtqatqqacqacqcaaaatcatcgaacaagqcacacacgaacaactgatgtcc gcataa

Figure 15 A

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catcatcgtgctggacgccggcaagatcgtcgagcacgggccgcacagcgagctgttggccgccaacgg

cgctctacaacatgcagttccgcgaggactga

Figure 15 B